		P25345		,,,		WINTS	_	492	34.9	40.5	33
	salmonella	085304		•	SALDU	PEPD		433		4 ٥	32
	mycoplasma	P75095		~			_	623	•	41	30
	caenorhabdi	021950			CASEL	SBP		. 576		41	29
	helicobacte	Q9z112			HELPJ	COAE		196		4.	27
	alligator m	P02200			ALLMI FIG	MYG	- -	154	35. B	41.	26
	rattus norv	P42346				FRAP		2549		4.	22
	homo sa	P42345			HUMAN	FRAP	۰,	2549		42	23
	bacillus su	P13267			BACSU	DPO3		1437		4 4	32
		Q9pc45			XYLFA	MSRA		216		4.	20
	archaeoglob	030130		_		PYRB		299		Ν,	19
	caenorhabdi	020701		•	CAEEL	GBA5		385		4. 4	18
	vibrio chol	P23247				DHAS		337		. Δ	16
	escherichia	P39370				SHLA	, ,,	326	37.5		15
	bovine herp	P12640			HSVBC	VGLB.		932		4 4 4 4	1 1 3
	sacchar	P48743			YEAST	RFXL		811		. 4	12
		P08266				RPB2		1176		44.5	= :
	methanosarc	QBthl2			METAC	PYRB		308	30.4	4 4	10 4
	sus scrofa	028920			and a	FRAP		127		4	, co
	saccharomyc	P23466			SACKL	CYA		1839		46	7
	mycobacteri	8 590 10	_		YD27_MYCTU	YD27	μ	737	39.7	46	σ,
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Transmembrane; Antigen.
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VGLB_HSV1K	VGLB_HSV11	VGLB_HSV1F	PLSB_XYLFA	VGLB_VZVD	HRPI_PSESY	PARC_BORBU	Clia_RAT	MNN9_YEAST	PLC_LISMO	YNUO YEAST	GUAN_RAT	
P06437	P10211	P06436	Q9pej7	P09257	P35655	051066	P14137	P39107	P34024	P40165	P28902	
herpes simp	herpes simp	herpes simp	xylella fas	-	pseudomonas	borrelia bu	rattus norv	saccharomyc	listeria mo	saccharomyc	rattus norv	

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ALIGNMENTS

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STEA_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

REDILINES-2015-271; PubMed=10588738;

HUBERT R.S., Vivanco I., Chen B., Rastegar S., Leong K.,

HICHERT R.S., Vivanco I., Chen B., Rastegar S., Leong K.,

Jakobovits A., Saffran D.C., Afar D.B.H.,

AFARTON B.H.,

AFARTON B.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SHISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license egreenent (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (ULL-2001) to the EMBL/GenBank/DDBJ databases.
-i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-i- TISSUE SPECIFICITY; HIGHLY EXPRESSED IN PROSTATE TUMOSS.
                                                                                                                                                                                                                                                                    EMBL; AF186249; AAF17479.1;
EMBL; AC005053; AAC79150.1;
EMBL; AC004969; AAD15620.1;
EMBL; BC011807; AAH11802.1;
Genew; HGNC:11378; STEAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STEAP OR STEAP1.
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Submitted (JUN-1998)
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)98) to the EMBL/GenBank/DDBJ databases
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RESULT 2
CIXG_HAEIN
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CixXg protein [Includes: Apo-citrate Jyase phosphoribosyl-dephosphorok transferses (EC 2.7.7.) (Apo-AEP nucleodity/transferses) 2.7.5. (phosphoribosyl)-3.-dephosphocoenzyme-A synthase (EC 4.2...) (2.3.1-cir)hosphoribosyl)-3. dephospho-CoA synthase).
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P44458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-Rd / KW20 / ATCC 51907;
MEDLINE-95350630, PubMed-7542800;
MEDLINE-95350630, Pubmed-7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                   the Buropean Bioinformatice Institute, There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this Etatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 269:496-512(1995).
-!- FUNCTION: BIFUNCTIONAL ENZYME THAT CATALYZES FORMATION OF 2-(5''-
                                                                     DOMAIN
                                                                                                                                                                                                                                        TIGR; HI0021, -
                                                                                                                                                                                                                                                        EMBL; U32687; AAC21699.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae.
                                                                                                                                           Complete
                                                                                                                                                                                      Pfam; PF01874; CitG;
                                                                                                                                                                  Transferase; Nucleotidyltransferase; Lyase; Multifunctional enzyme;
                       EQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRIPHOSPHORIBOSYL)-1'-DEPHOSPHOCOENZYME-A, AND THEN THE TRANSFER OF THIS PROSTHETIC GROUP PRECURSOR TO THE APO-ACYL CARRIER PROTEIN (GAMMA CHAIN) OF THE CITRATE LYASE TO YIELD THE HOLD-ACYL CARRIER PROTEIN (BY SIMILARITY).

PROTEIN (BY SIMILARITY)

CAPALYTIC ACTIVITY: Dephospho-COA + ATP = 2-(5''-
CAPALYTIC ACTIVITY: Dephospho-COA + adenine.
SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE CITY FAMILY.
SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE CITY FAMILY.
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                                           DEPHOSPHO-COA TRANSFERASE.
2-(5',-TRIPHOSPHORIBOSYL)-3'-
DEPHOSPHOCOENZYME-A SYNTHASE.
                                                                                                                    APO-CITRATE LYASE PHOSPHORIBOSYL-
                          4467221C3DB58A96
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RESULT 4
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Q9HQG0;
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Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Shorgna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Iesthauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Maddocks D.G., Jablonski P.E., Cherkson M.P., Donnis P.P., Omer A.D.,
Isenbarder T.A., Peck R.F., Pohlschroder M., Spondich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Ebharder H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
"Genome sequence of Halbacterium species M.RC-1."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HALNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to methionine (By similarity).

-i- CATALYTIC ACTIVITY: Protein L-methionine + oxidized thioredoxin protein L-methionine S-oxide + reduced thioredoxin.

-i- SIMILARITY: BELONGS TO THE MSRA MET SULFOXIDE REDUCTASE FAMILY.

    -i- FUNCTION: Has an important function as a repair enzyme for
proteins that have been inactivated by oxidation. Catalyzes the
reversible oxidation-reduction of methionine sulfoxide in prote

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ls-tJN-2002 [Rel. 41, Last annotation update)
Reptide methionine sulfoxide reductase merA (EC 1.8.4.6) (Protein-
methionine-S-oxide reductase) (Peptide Met(O) reductase).
                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                             Oxidoreductase; Complete proteome.
ACT_SITE 12 12 BY SI
                                                                                                                                                                                                                                                                                                                                                               TIGRFAMs; TIGRO0401; msrA; 1.
                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD003489; PMSR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002569; PMSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P54149; 1FVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE005045; AAG19555.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
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L5-JUN-2002
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                                                                                                135 ETFYPAAEKHQNYFEKNP 152
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                                                                                                                                              2 EVIHPLATSHOOYFYKIP 19
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                                                                                                                                                                                         l Similarity
9; Conserv
                                                                                                                                                                                                                                                                                         177 AA;
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Pred. No. 0.66;
                                                                                                                                                                                                                    Score 49; DB 1
Pred. No. 0.81;
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Maximum Match 100%
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Maximum DB
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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DAPD BUCAL
YC73 METUA
SYV CHLPN
YAW, RHISISN
NCM2 HUMAN
NCM3 HUMAN
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WormPop; ZK512.3; CE00409.
InterPro; IPR002111; Cat_channel
SEQUENCE 1418 AA; 159237 MW;
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MEDLINE=94150718; PubMed=7906398;
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Rhabditidae; Peloderinae; Caenorhabditis.
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ED-11 OR ZK512.3
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elegans.";
   Minor teichoic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            his SMISS-PROT entry is copyright. It is produced through a collaboration newson the Swiss Institute of Buoinformatics and the EWBL outstation in Buopean Bidinformatical Institute of There are no testrictions on it use by non-profit institutions as long as its content as in non-commercial commencation of the statement is not trempwed. Usage by and for commercial commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 218
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                                                                                                                                                                                                                         Query Match
                                                                                                                                                                       Matches
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Interpro; IPR001173; Glycos transf_2; I.
Pfam; PF00535; Glycos transf_2; I.
Transferase; Glycos/Itransferase; Com
Fransferase; Glycos/Itransferase; Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U13979; AAA73513.1;
EMBL; Z99122; CAB15585.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 390:249-256(1997)
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Submitted (AUG-1994)
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Pred. No. 3.7;
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FA66495488C2C62F CRC64;
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4.77

Length 900

0, Gaps

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Kunst F. Ogasawar M., Mosser I., Albertini A.M., Alloni G.,
RA Kunst F. Ogasawar M., Mosser P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Bronillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connetton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Butlan K.D., Errington J., Fabret C., Ferrari E., Fouldger D.,
RA Chim S.Y., Calaser P., Goffeau A., Golightly B.J., Grandi G.,
RA Chim S.Y., Calaser P., Goffeau A., Golightly B.J., Grandi G.,
RA Guiseppi G., Guy B.J., Hage K., Haisech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Lubber J., Lazarevic V.,
RA Guiseppi G., Guy B.J., Hage K., Haisech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Lauber J., Lazarevic V.,
RA Guiseppi G., Guy B.J., Hardinois S., Lauber J., Lazarevic V.,
RA Hilbert N., Levine A., Liu H., Masuds S., Lauber J., Lazarevic V.,
RA Hollado R.P., Mizuno M., Moestl D., Nekai S., Noback M.,
Moone D., O'Reilly M., O'Gawat M., Golywat A., Guidge B., Paak M.H.,
RA Woone D., O'Reilly M., O'Gawat M., Golywat A., Sercor D., Ray M., Reynolds S.,
RA Rasger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Rasger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie S.,
RA Rasger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie S.,
RA Sarokin A., Tacconi E., Takagi T., Takahashi H., Takematu K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Vashikawa H., Danchin A.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yosnica K.,
Ra Wibrit R., Wedler E., Medler H., Meitzenegger T.,
RA Wilhers P., Mipat A., Yanamoto H., Yanane K., Yasumo K.,
Ra The Complete genome sequence of the Gram-positive bacterium Bacillus
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillales; Bacillaceae; Bacillus.
                                                                                                                       IN THE BIOSYNTHESIS OF GALACTOSAMINE-CONTAINING
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Run on:
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March 26, 2003, 16:38:14 ; Search time 4.36047 Seconds (without alignments) 142.679 Million cell updates/sec
                                                                                                                                                                                      Copyright
                                                                                                                                                                                   GenCore version 5.1.4_p5_4578
(c) 1993 - 2003 Compugen Ltd.
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Scoring table: Perfect score: sequence: BLOSUM62 Gapop 10.0 , US-10-010-667A-21 93 1 WIDIKQFVWYTPPTF Gapext 0.5 15

number of hits satisfying chosen parameters: 112892 seqs, 41476328 residues

112892

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Maximum Minimum DB seq length: 0
DB seq length: 2000000000

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Deci, 1						**
No.			ength	BG	ID	iption
1	93	100.0	339	- 5	STEA HUMAN	Q9uhe8 homo sapien
2	52,	55.9	458	_	AGLE_RHIME	rhiz
w	45	48.4	865	_	ENV_HV1RH	P04579 human immun
4	43.5	46.8	1167	_	WC1_NEUCR	
u	42	45.2	346	۳	OPSP ICTPU	042266 ictalurus p
o	42	45.2	396	۳,	YJR1_YBAST	saccharomy
	42	45.2	583	_	ERF2 YEAST	
	42	45.2	795	_	TLR1 MOUSE	
	42	45.2	847	٢	ENV HV1S1	P19550 human immun
10	41.5	44.6	224	_	YN89 YEAST	
11	41	44.1	405	μ	WCAD ECOLI	
12	41	44.1	430	_	PUCK_BACSU	
13	41	44.1	703	μ	ARYB MANSE	P14297 manduca sex
14	41	44.1	843	Н	ENV_HV1Y2	P35961 human immun
15	41	44.1	854	Ļ	ENV_SIVCZ	P17281 chimpanzee
16	41	44.1	856	μ	ENV_HV1ZH	
17	41	44.1	1509	μ	MYSN_ACACA	a
18	41	44.1	1628	μ	NAGH_CLOPE	
19	40	43.0	226	,	HA2P_RABIT	
20	40	43.0	847	-	ENV_HV1W2	_
21	40	43.0	853	_	ENV_HV1Z2	P12487 human immun
22	40	43.0	855	μ	ENV_HV1Z6	P04580 human immun
23	40	43.0	856	بر	ENV_HV1MN	P05877 human immun
24	39.5	42.5	263	μ	MPL1_LOLPR	P14946 lolium pere
25	9	42.5	263	,	MPP1_PHLPR	phleum
26	9	42.5	265	_	MPH1_HOLLA	
27	39.5	42.5	269	_	MPA1_PHAAQ	0
28	9	42.5	551	μ	YABN_ECOLI	
29	9	42.5	701	_	ACSA_HUMAN	Q9nr19 homo sapien
30	39	41.9	210	_	SSH5_YEAST	
31	39	41.9	223	_	CDR1_HUMAN	
32		41.9	282		Y765 HABIN	
33	39	41.9	289	_	MIM3 METJA	Q58015 methanococc

				11				17	8	5	4	
38	38	38	38	38	<u>۵</u>	8.5	39	39	39	39	39	
40.9	40.9	40.9	40.9	40.9	40.9	41.4	41.9	41.9	41.9	41.9	41.9	
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Q9r237	Q9wvi9 mus musculu	Q61496		067876 aquifex aeo	P06008	. P33353	P05879	_	P33137	P92668	Q9kdm4	

ALIGNMENTS

RESULT 1	UT 1	
STEA	STEA HUMAN	
Ā	STEA HUMAN STANDARD; PRT; 339 AA.	
č	Q9UHEB; O95034;	
3	16-OCT-2001 (Rel. 40, Created)	
ဌ	16-OCT-2001 (Rel. 40, Last sequence update)	
7	15-JUN-2002 (Rel. 41, Last annotation update)	
B	Six transmembrane epithelial antigen of prostate.	
2	STEAP OR STEAP1.	
8	Homo sapiens (Human).	
ಗ	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
೧	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo	
×	NCBI_TaxID=9606;	
R	[1]	
RP	SEQUENCE FROM N.A.	
2	MEDLINE=20056277; PubMed=10588738;	
R	Hubert R.S., Vivanco I., Chen E., Rastegar S., Leong K.,	
R	Mitchell S.C., Madraswala R., Zhou Y., Kuo J., Raitano A.B.,	
Ŗ	Jakobovits A., Saffran D.C., Afar D.E.H.;	
RT	"STEAP: a prostate-specific cell-surface antigen highly expressed in	
R	human prostate tumors.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 96:14523-14528(1999).	
R	[2]	
RP	SEQUENCE FROM N.A.	
S	Abu-Threideh J., Stoneking T., Langston Y., Maupin R.;	
RL	Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.	
R	[3]	
3	CECHENICE EBON N.	

the Buropean Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commentariate requires a license apresent (See http://www.isb-sib.ch/annoor send an email to licenseaesib-sib.ch). This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -(See http://www.isb-sib.ch/announce/

TISSUE-Skin;

EMBL; AF186249; AAF17479.1; EMBL; AC005053; AAC79150.1; EMBL; AC004969; AAD15620.1; EMBL; BC011802; AAH11802.1; Genew; HGNC:11378; STEAP ALT_INIT.

MIM; 604415; -. Antigen

SOUTH THE REAL PROPERTY OF THE TRANSMEM TRANSMEM SEQUENCE TRANSMEM TRANSMEM TRANSMEM Transmembrane; TRANSMEM 7 339 AA; 119 164 218 258 39851 MW; POTENTIAL.
POTENTIAL.
POTENTIAL.
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POTENTIAL.
POTENTIAL. 55443A170C870387 CRC64;

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REMBL, AP045-0-,

REMBL, AP045-0-,

REMBL, ALPO1704; CAC4526...,

REMBL, ALPO1704; CAC4526...,

REMBL, ALPO1804; CAC4526...,

REMBL, AP00567; SBP_baccl.

REMBL, AP00567; SBP_baccl.

REMBL, AP005671; Transport; Periplasmic, Signal; Complete proteome.

SUGAT transport; Transport; Periplasmic, Signal; Complete proteome.

WEMPLA, CALLONGE, AP076811, CAMPLA, CALLONGE, BROTEN, AGLE.

AP0703 MW, ETATPB157C2FC291 CRC64;

Length 458;
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Best Local S
Matches 15
                                                               Matches
                                                                                      Query Match
Best Local
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Boistard D. Becker A., Bourry M., Cadieu E., Dreano S., Gloux S.,
Godrie T., Geffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Forteelle D., Pueller A., Purnelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Watdner S., Galibert F.;
Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium mellioti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001)
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001)
PROC. THE SINDING-PROTEIN-DEFENDENT TRANSPORT SYSTEM
FOR ALPHA-GLUCOSIDES SUCH AS SUCROSE, MALTOSE AND TREHALOSE.
SUBCELLIAL BLOCATION. PERILBASTIC (Probable)
-- SINGLARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGLE RHIME
Q9Z3R5;
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                           his SMASS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatice and the ERMI contensation the European Bioinformatice Institute. There are no testicitions on use by non-profit institutions as long as its content ictions of modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/announcer.ch/).
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15-JUN-2002 (Rel. 41, Last seq
15-JUN-2002 (Rel. 41, Last and
15-JUN-2002 (Rel. 41, Last and
Alpha-glucosides-binding perip
AGLE OR R00695 OR SMC03061.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Willis L.B., Walker G.C.;
"A novel sinorhizobium meliloti operon encodes an alpha-glucosidase
"A novel sinorhizobium sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99328961;
Willis L.B., Walke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phizobium meliloti (Sinorhizobium meliloti)
poteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277
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                                                               Similarity
8; Conserv
                                                               Conservative
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llarity 100.0%;
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Pred. No. 7.8e-08;
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                                                           ed. No. 0.45;
Mismatches
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Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F
"Identification and characterization of conserved and variable
regions in the envelope gene of HTLV-III/LAV, the retrovirus of
AIDS.";
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13-AUG-1987 (Rel. 05, Last sequence update)
15-UU-1997 (Rel. 05, Last annotation update)
15-UU-1999 (Rel. 08, Last annotation update)
Envelope polyprotein (GP160 precursor (Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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InterPro; IPR000777; GP120.
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between the Swiss Institute of Bioinformatics and the EMBL
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Starcich B.R., Hahn B.H., Shaw G.M.,
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